



SEQUENCE LISTING

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TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: ARATHOON, P.
CAPTEE, P.J.
MEFCHANT, A.M.
PRESTA, L.G.

(ii) TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
HAVING HETEROMULTIMERIC AND COMMON
COMPONENTS

(iii) NUMBER OF SEQUENCES: 28

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 07-Mar-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/070,416
(B) FILING DATE: 30-APR-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Conley, Deirdre L.
(B) REGISTRATION NUMBER: 36,487
(C) REFERENCE/DOCKET NUMBER: P1099R2C1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-2000

A. NAME: Conley, Deirdre L.
B. STREET: 1 DNA Way
C. CITY: South San Francisco
D. STATE: California
E. COUNTRY: USA
F. ZIP: 94080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTTCCCGA GATGGGGGCA GGTGTCACAC CTGTGG 36

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCTTCCCGA CATGGGGGCA G 21

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTCATCTCA CACCGGGATG G 21

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTGCTCATA CATTCACGGG ATGG 24

CTTGCTCATA CATTCACGGG ATGG 24

CTTGCTCATA CATTCACGGG ATGG 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCTTCCCGA GATGGGGGAC AGGTGTACAC 30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (E) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCCGTCGGAA CACAGCACGG G 21

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (E) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGGAGTCT AGAACGGGAG GCGTGGTACA GTAGTTGTT 39

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (E) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCGGAGTCT AGAACGGGAG GACAGGTCTT GTA 33

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (E) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGGAGTCT AGACAGGGAG G 11

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCGTCGGAG CTCAGCACGG G 21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGAGGCGTG GTGCTGTAGT TGTT 24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGAGGTGC TGGGCTCGGT GGGCTTGTGT GAGTTTGT 38

SEQUENCE LISTING

SEQUENCE LISTING:
1. NAME OF SEQUENCE: 1.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACGCGTACG CTCTGAAAAT GCGGACCG AACCGTTTTC GTGGTAAAGA 50
TCTGGCTGCA CACTACGGCC AGCCGCGGGA ACCTCAGGTG TATACCCTGC 100
CACCGTCTCG AGAAGAAATG ACTAAAAACC AGGTCTCTCT GTGGTGCCTG 150
GTCAAAGGTT TCTATCCGAG CGATATCGCC GTGGAATGGG AAAGCAACGG 200
TCAACCGGAA AACAAC TACA AAACCACTCC ACCGGTGCTG GATTCTGATG 250
GCTCCTTCTT TCTGTATTCG AAGCTGACCG TTGACAAAAG CCGTTGGCAG 300
CAAGGCAACG TTTTCAGCTG TTCTGTTATG CACGAGGCCT TGCACAACCA 350
CTACACCCAG AAAAGCCTGT CCCTGTCTCC CGGGAATAA GCTGAGGCTC 400
CTCTAGAGGT TGAGGTGATT TTATGAAAAA GAATATCGCA TTTCTTCTTG 450
CATCTATGTT CGTTTTTCT ATTGCTACAA ACGCGTACGC TGGGCAGCCC 500
CGAGAACCAAC AGGTGTACAC CCTGCCCCCA TCCCGGGAAG AGATGACCAA 550
GAACCAGGTA AGCTTGTA CT GCTGGTCAA AGGCTTCTAT CCCAGCGACA 600
TGGCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC 650
ACGCTCCCG TGCTGGACTC CGACGGCTCC TTCTCCTCT ACAGCTTTCT 700
CACCGTCGAC AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG 750
TGATGCATGA GGTCTGCAAC AACCACTACA CGCAGAAGAG CCTCTCCCTG 800
TCTCCGGCTA AATAGGGCT C 821

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(P) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Protein Name: ...
...
...

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
1 5 10 15
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
35 40 45
Lys Leu Thr Val Leu
50

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
1 5 10 15
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
35 40 45
Lys Leu Thr Val Leu
50

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
1 5 10 15

Lys Leu Thr Val Leu
50

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(E) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Asn Arg Phe Ser Gly Ser Lys Xaa Gly Asn Thr Ala Ser Leu
1 5 10 15
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
35 40 45
Lys Leu Thr Val Leu
50

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(E) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
1 5 10 15
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
35 40 45
Lys Leu Thr Val Leu
50

1 234567891011121314151617181920212223242526272829303132333435363738394041424344454647484950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

[illegible]

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(E) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

[illegible]

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

Thr Ala Val Tyr Tyr Cys Ala Arg Val Asp Leu Glu Asp Tyr Gly
 35 40 45

Ser Gly Ala Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 50 55 60

Ser Ser
 62

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile
 1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr
 20 25 30

His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45

Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 65 70 75

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 80 85 90

Tyr Ser Asn Tyr Phe Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu
 95 100 105

Ile Lys
 107

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

Lys	Asp	Leu	Ala	Ala	His	Tyr	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	20	25	30
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	35	40	45
Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	50	55	60
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	65	70	75
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	80	85	90
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	95	100	105
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	110	115	120
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Xaa	Met	Lys	Lys	Asn	Ile	125	130	135
Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	Ser	Ile	Ala	Thr	Asn	140	145	150
Ala	Tyr	Ala	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	155	160	165
Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Tyr	Cys	170	175	180
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	185	190	195
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	200	205	210
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Phe	Leu	Thr	Val	215	220	225
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	230	235	240

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAGGTGCAGC TGGTGCAGTC TGGGGGAGGC TTGGTCCGGC CCGGGGGGTC 50
CCTGAGTCTC TCCTGTGCAG TCTCTGGAAT CACCCTCAGG ACCTACGGCA 100
TGCACTGGGT CCGCCAGGCT CCAGGCAAGG GGCTGGAGTG GGTGGCAGGT 150
ATATCCTTTG ACGGAAGAAG TGAATACTAT GCAGACTCCG TGCAGGGCCG 200
ATTCACCATC TCCAGAGACA GTTCCAAGAA CACCCTGTAT CTGCAAATGA 250
ACAGCCTGAG AGCCGAGGAC ACGGCTGTGT ATTACTGTGC GAGAGGAGCA 300
CATTATGGTT TCGATATCTG GGGCCAAGGG ACAATGGTCA CCGTCTCGAG 350
TGGTGGAGGC GGTACAGGCG GAGGTGGCAG CGGCGGTGGC GGATCGGACA 400
TCCAGATGAC CCAGTCTCCT TCCACCCCTGT CTGCATCTAT TGGAGACAGA 450
GTCAACATCA CCTGCCGGGC CAGCGAGGGT ATTTATCACT GGTGGGCTG 500
GTATCAGCAG AAGCCAGGGA AAGCCCCCTAA ACTCCTGATC TATAAGGCCT 550
CTAGTTTAGC CAGTGGGGCC CCATCAAGGT TCAGCGGCAG TGGATCTGGG 600
ACAGATTCCA TCTCAGCAT CAGCAAGCTG CAGCCTGATG ATTTGCAAC 650
TTATTACTGC CAGCAAGATA GTAATTATCC GGTCACTTTC GGCGGAGGGA 700
CCAAGCTGGA GATCAAA 717

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: Nucleic Acid

CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGTTATGAAA 100
TGAAGTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGGT 150
ATTAGTGGTA GTGGTGGTAG CACATACTAC GCAGACTCCG TGAAGGGCCG 200
GTTCAACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 250
ACAGACTGAG AGCTGAGGAC ACGGCTGTGT ATTACTGTGC GAGAGATAAT 300
GGGTGGGAAC TAACGGACTG GTACTTCGAT CTCTGGGGCC GGGGGACAAT 350
GGTCACCGTC TCCTCAGGTG GAGGCGGTTC AGGCGGAGGT GGCAGCGGCG 400
GTGGCGGATC GGACATCCAG ATGACCCAGT CTCCTTCCAC CCTGTCTGCA 450
TCTATTGGAG ACAGAGTCAC CATCACCTGC CGGGCCAGTG AGGGTATTTA 500
TCACTGGTTG GCCTGGTATC AGCAGAAGCC AGGGAAAGCC CCTAAACTCC 550
TGATCTATAA GGCTCTAGT TTAGCCAGTG GGGCCCCATC AAGGTTCAGC 600
GGCAGTGGAT CTGGGACAGA TTCACTCTC ACCATCAGCA GCCTGCAGCC 650
TGATGATTTT GCAACTTATT ACTGCCAACA ATATAGTAAT TATCCGCTCA 700
CTTTCGGCGG AGGGACCAAG CTGGAGATCA AA 732